

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/936,190

DATE: 10/04/2001  
TIME: 15:29:01

Input Set : A:\Nobf5002.app  
Output Set: N:\CRF3\10042001\I936190.raw

3 <110> APPLICANT: STEELE, Christopher L.  
4 DIXON, Richard A.  
6 <120> TITLE OF INVENTION: GENETIC MANIPULATION OF ISOFLAVONOID  
8 <130> FILE REFERENCE: 11137/05006  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/936,190  
C--> 11 <141> CURRENT FILING DATE: 2001-09-13  
13 <150> PRIOR APPLICATION NUMBER: 60/123,267  
14 <151> PRIOR FILING DATE: 1999-03-08  
16 <160> NUMBER OF SEQ ID NOS: 5  
18 <170> SOFTWARE: PatentIn Ver. 2.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 1717  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Glycine max  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (36)..(1598)  
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31 Met Leu Leu Glu Leu Ala  
32 1 5  
34 ctt ggt tta ttg gtt ttg gct ctg ttt ctg cac ttg cgt ccc aca ccc 101  
35 Leu Gly Leu Leu Val Leu Ala Leu Phe Leu His Leu Arg Pro Thr Pro  
36 10 15 20  
38 act gca aaa tca aaa gca ctt cgc cat ctc cca aac cca cca agc cca 149  
39 Thr Ala Lys Ser Lys Ala Leu Arg His Leu Pro Asn Pro Pro Ser Pro  
40 25 30 35  
42 aag cct cgt ctt ccc ttc ata gga cac ctt cat ctc tta aaa gac aaa 197  
43 Lys Pro Arg Leu Pro Phe Ile Gly His Leu His Leu Lys Asp Lys  
44 40 45 50  
46 ctt ctc cac tac gca ctc atc gac ctc tcc aaa aaa cat ggt ccc tta 245  
47 Leu Leu His Tyr Ala Leu Ile Asp Leu Ser Lys Lys His Gly Pro Leu  
48 55 60 65 70  
50 ttc tct ctc tac ttt ggc tcc atg cca acc gtt gtt gcc tcc aca cca 293  
51 Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro  
52 75 80 85  
54 gaa ttg ttc aag ctc ttc ctc caa acg cac gag gca act tcc ttc aac 341  
55 Glu Leu Phe Lys Leu Phe Leu Gln Thr His Glu Ala Thr Ser Phe Asn  
56 90 95 100  
58 aca agg ttc caa acc tca gcc ata aga cgc ctc acc tat gat agc tca 389  
59 Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Ser Ser  
60 105 110 115  
62 gtg gcc atg gtt ccc ttc gga cct tac tgg aag ttc gtg agg aag ctc 437  
63 Val Ala Met Val Pro Phe Gly Pro Tyr Trp Lys Phe Val Arg Lys Leu  
64 120 125 130  
66 atc atg aac gac ctt ctc aac gcc acc act gta aac aag ttg agg cct 485  
67 Ile Met Asn Asp Leu Leu Asn Ala Thr Thr Val Asn Lys Leu Arg Pro

ENTERED

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68 135          140          145          150
70 ttg agg acc caa cag atc cgc aag ttc ctt agg gtt atg gcc caa ggc 533
71 Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu Arg Val Met Ala Gln Gly
72          155          160          165
74 gca gag gca cag aag ccc ctt gac ttg acc gag gag ctt ctg aaa tgg 581
75 Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr Glu Glu Leu Leu Lys Trp
76          170          175          180
78 acc aac agc acc atc tcc atg atg atg ctc ggc gag gct gag gag atc 629
79 Thr Asn Ser Thr Ile Ser Met Met Met Leu Gly Glu Ala Glu Glu Ile
80          185          190          195
82 aga gac atc gct cgc gag gtt ctt aag atc ttt ggc gaa tac agc ctc 677
83 Arg Asp Ile Ala Arg Glu Val Leu Lys Ile Phe Gly Glu Tyr Ser Leu
84          200          205          210
86 act gac ttc atc tgg cca ttg aag cat ctc aag gtt gga aag tat gag 725
87 Thr Asp Phe Ile Trp Pro Leu Lys His Leu Lys Val Gly Lys Tyr Glu
88 215          220          225          230
90 aag agg atc gac gac atc ttg aac aag ttc gac cct gtc gtt gaa agg 773
91 Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe Asp Pro Val Val Glu Arg
92          235          240          245
94 gtc atc aag aag cgc cgt gag atc gtg agg agg aga aag aac gga gag 821
95 Val Ile Lys Lys Arg Arg Glu Ile Val Arg Arg Arg Lys Asn Gly Glu
96          250          255          260
98 gtt gtt gag ggt gag gtc agc ggg gtt ttc ctt gac act ttg ctt gaa 869
99 Val Val Glu Gly Glu Val Ser Gly Val Phe Leu Asp Thr Leu Leu Glu
100          265          270          275
102 ttc gct gag gat gag acc atg gag atc aaa atc acc aag gac cac atc 917
103 Phe Ala Glu Asp Glu Thr Met Glu Ile Lys Ile Thr Lys Asp His Ile
104          280          285          290
106 aag ggt ctt gtt gtc gac ttt ttc tcg gca gga aca gac tcc aca gcg 965
107 Lys Gly Leu Val Val Asp Phe Phe Ser Ala Gly Thr Asp Ser Thr Ala
108 295          300          305          310
110 gtg gca aca gag tgg gca ttg gca gaa ctc atc aac aat cct aag gtg 1013
111 Val Ala Thr Glu Trp Ala Leu Ala Glu Leu Ile Asn Asn Pro Lys Val
112          315          320          325
114 ttg gaa aag gct cgt gag gag gtc tac agt gtt gtg gga aag gac aga 1061
115 Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser Val Val Gly Lys Asp Arg
116          330          335          340
118 ctt gtg gac gaa gtt gac act caa aac ctt cct tac att aga gca atc 1109
119 Leu Val Asp Glu Val Asp Thr Gln Asn Leu Pro Tyr Ile Arg Ala Ile
120          345          350          355
122 gtg aag gag aca ttc cgc atg cac ccg cca ctc cca gtg gtc aaa aga 1157
123 Val Lys Glu Thr Phe Arg Met His Pro Pro Leu Pro Val Val Lys Arg
124          360          365          370
126 aag tgc aca gaa gag tgt gag att aat gga tat gtg atc cca gag gga 1205
127 Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly Tyr Val Ile Pro Glu Gly
128 375          380          385          390
130 gca ttg att ctc ttc aat gta tgg caa gta gga aga gac ccc aaa tac 1253
131 Ala Leu Ile Leu Phe Asn Val Trp Gln Val Gly Arg Asp Pro Lys Tyr
132          395          400          405

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134 tgg gac aga cca tcg gag ttc cgt cct gag agg ttc cta gag aca ggg 1301
135 Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu Arg Phe Leu Glu Thr Gly
136          410          415          420
138 gct gaa ggg gaa gca ggg cct ctt gat ctt agg gga caa cat ttt caa 1349
139 Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu Arg Gly Gln His Phe Gln
140          425          430          435
142 ctt ctc cca ttt ggg tct ggg agg aga atg tgc cct gga gtc aat ctg 1397
143 Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu
144          440          445          450
146 gct act tcg gga atg gca aca ctt ctt gca tct ctt att cag tgc ttc 1445
147 Ala Thr Ser Gly Met Ala Thr Leu Leu Ala Ser Leu Ile Gln Cys Phe
148 455          460          465          470
150 gac ttg caa gtg ctg ggt cca caa gga cag ata ttg aag ggt ggt gac 1493
151 Asp Leu Gln Val Leu Gly Pro Gln Gly Gln Ile Leu Lys Gly Gly Asp
152          475          480          485
154 gcc aaa gtt agc atg gaa gag aga gcc ggc ctc act gtt cca agg gca 1541
155 Ala Lys Val Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala
156          490          495          500
158 cat agt ctt gtc tgt gtt cca ctt gca agg atc ggc gtt gca tct aaa 1589
159 His Ser Leu Val Cys Val Pro Leu Ala Arg Ile Gly Val Ala Ser Lys
160          505          510          515
162 ctc ctt tct taattaagat catcgtcatc atcatcatat gtaatatatta 1638
163 Leu Leu Ser
164          520
166 ctttttgtgt gttgataatc atcatttcaa taagggtctca ttcactctact ttttatgaag 1698
168 tatataagcc cttccatgc 1717
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 521
173 <212> TYPE: PRT
174 <213> ORGANISM: Glycine max
176 <400> SEQUENCE: 2
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180 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
181          20          25          30
183 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
184          35          40          45
186 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
187          50          55          60
189 Lys Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
190 65          70          75          80
192 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
193          85          90          95
195 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
196          100          105          110
198 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
199          115          120          125
201 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
202          130          135          140

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204 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
205 145 150 155 160
207 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
208 165 170 175
210 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
211 180 185 190
213 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
214 195 200 205
216 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
217 210 215 220
219 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
220 225 230 235 240
222 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
223 245 250 255
225 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
226 260 265 270
228 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
229 275 280 285
231 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
232 290 295 300
234 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
235 305 310 315 320
237 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
238 325 330 335
240 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
241 340 345 350
243 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
244 355 360 365
246 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
247 370 375 380
249 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
250 385 390 395 400
252 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
253 405 410 415
255 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
256 420 425 430
258 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
259 435 440 445
261 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
262 450 455 460
264 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
265 465 470 475 480
267 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
268 485 490 495
270 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
271 500 505 510
273 Ile Gly Val Ala Ser Lys Leu Leu Ser
274 515 520
278 <210> SEQ ID NO: 3

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279 <211> LENGTH: 523
280 <212> TYPE: PRT
281 <213> ORGANISM: Glycyrrhiza echinata
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288           20           25           30
290 Pro Pro Ser Pro Phe Phe Arg Leu Pro Ile Ile Gly His Met His Met
291           35           40           45
293 Leu Gly Pro Leu Leu His Gln Ser Phe His Asn Leu Ser His Arg Tyr
294           50           55           60
296 Gly Pro Leu Phe Ser Leu Asn Phe Gly Ser Val Leu Cys Val Val Ala
297   65           70           75           80
299 Ser Thr Pro His Phe Ala Lys Gln Leu Leu Gln Thr Asn Glu Leu Ala
300           85           90           95
302 Phe Asn Cys Arg Ile Glu Ser Thr Ala Val Lys Lys Leu Thr Tyr Glu
303           100          105          110
305 Ser Ser Leu Ala Phe Ala Pro Tyr Gly Asp Tyr Trp Arg Phe Ile Lys
306           115          120          125
308 Lys Leu Ser Met Asn Glu Leu Leu Gly Ser Arg Ser Ile Asn Asn Phe
309           130          135          140
311 Gln His Leu Arg Ala Gln Glu Thr His Gln Leu Leu Arg Leu Leu Ser
312 145           150          155          160
314 Asn Arg Ala Arg Ala Phe Glu Ala Val Asn Ile Thr Glu Glu Leu Leu
315           165          170          175
317 Lys Leu Thr Asn Asn Val Ile Ser Ile Met Met Val Gly Glu Ala Glu
318           180          185          190
320 Glu Ala Arg Asp Val Val Arg Asp Val Thr Glu Ile Phe Gly Glu Phe
321           195          200          205
323 Asn Val Ser Asp Phe Ile Trp Leu Phe Lys Lys Met Asp Leu Gln Gly
324           210          215          220
326 Phe Gly Lys Arg Ile Glu Asp Leu Phe Gln Arg Phe Asp Thr Leu Val
327 225           230          235          240
329 Glu Arg Ile Ile Ser Lys Arg Glu Gln Thr Arg Lys Asp Arg Arg Arg
330           245          250          255
332 Asn Gly Lys Lys Gly Glu Gln Gly Ser Gly Asp Gly Ile Arg Asp Phe
333           260          265          270
335 Leu Asp Ile Leu Leu Asp Cys Thr Glu Asp Glu Asn Ser Glu Ile Lys
336           275          280          285
338 Ile Gln Arg Val His Ile Lys Ala Leu Ile Met Asp Phe Phe Thr Ala
339           290          295          300
341 Gly Thr Asp Thr Thr Ala Ile Ser Thr Glu Trp Ala Leu Val Glu Leu
342 305           310          315          320
344 Val Lys Lys Pro Ser Val Leu Gln Lys Val Arg Glu Glu Ile Asp Asn
345           325          330          335
347 Val Val Gly Lys Asp Arg Leu Val Glu Ser Asp Cys Pro Asn Leu
348           340          345          350
350 Pro Tyr Leu Gln Ala Ile Leu Lys Glu Thr Phe Arg Leu His Pro Pro

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/936,190

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TIME: 15:29:02

Input Set : A:\Nobf5002.app

Output Set: N:\CRF3\10042001\I936190.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date